

MA61 - A part of the SCF E3 ubiquitin Ligase Complex

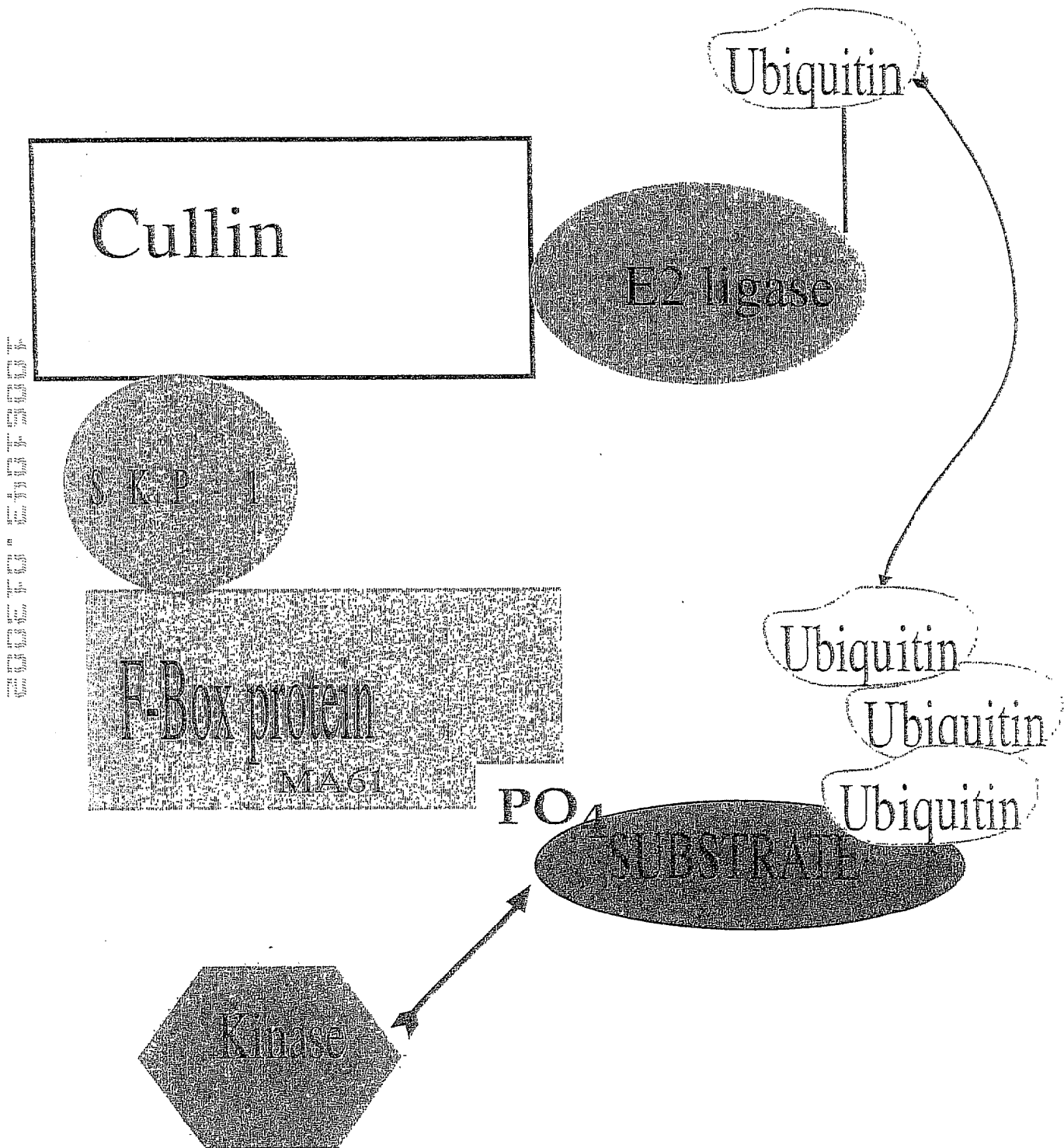


FIGURE 2
ClustalW Formatted Alignments

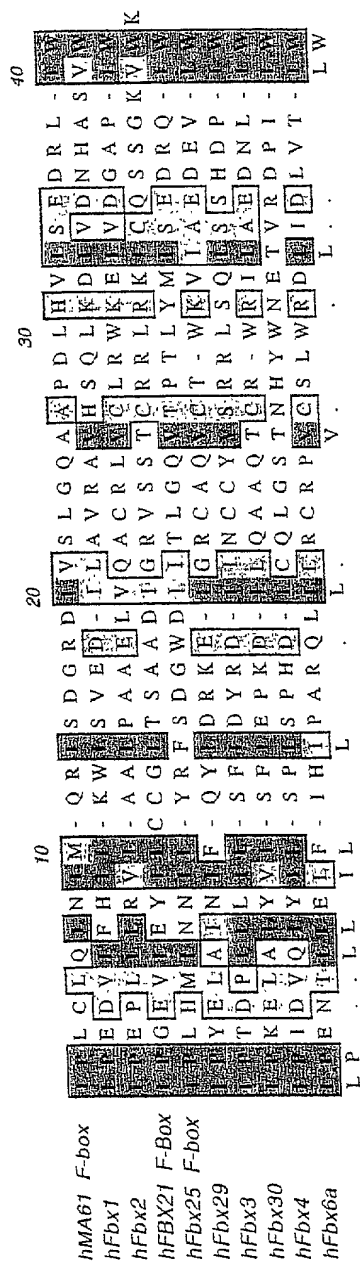
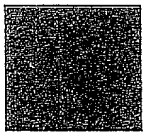
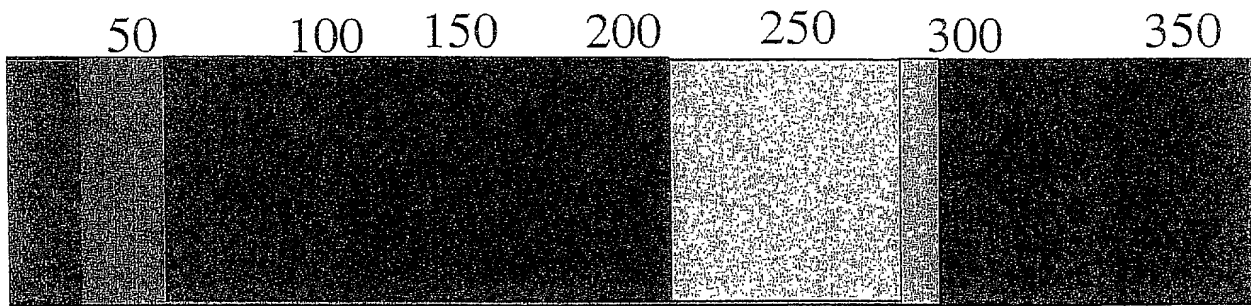
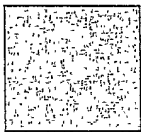


FIGURE 3

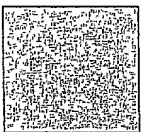
MA 61



Fbx25 Homology Domain (1-25; 86-360)



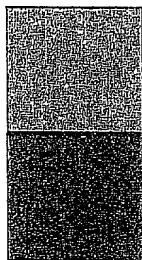
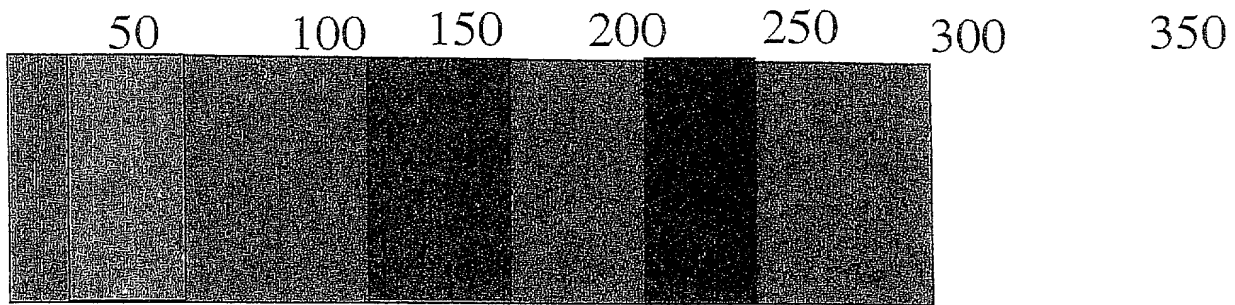
F-Box Domain (217-264)



Bipartite nuclear localization signal (262-279)

FIGURE 4

Human MURF 1 schematic



RING Finger Domain (26-82)

BBOX (121-163)



Spectrin Repeat (207-233)

ClustalW Formatted Alignments

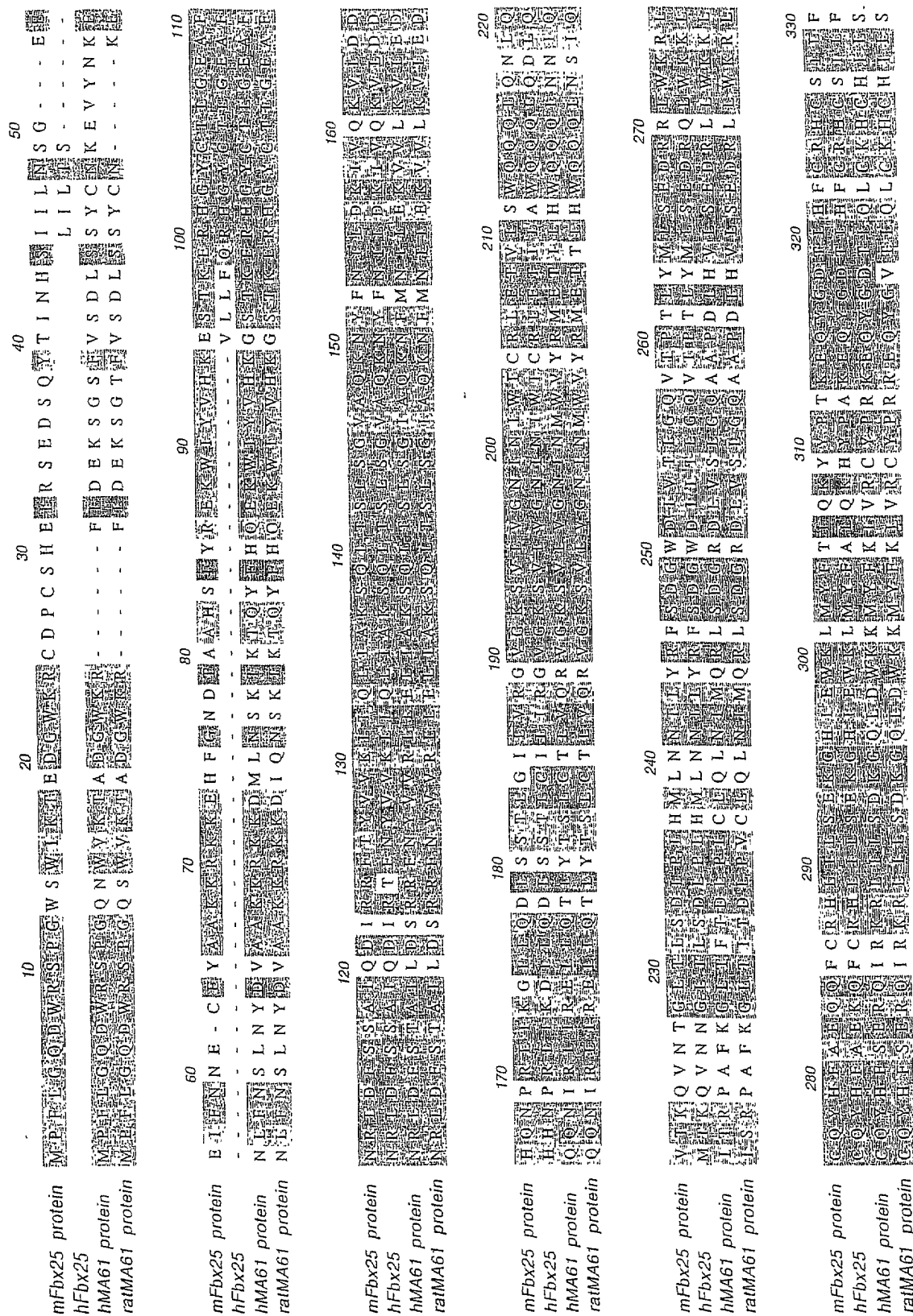
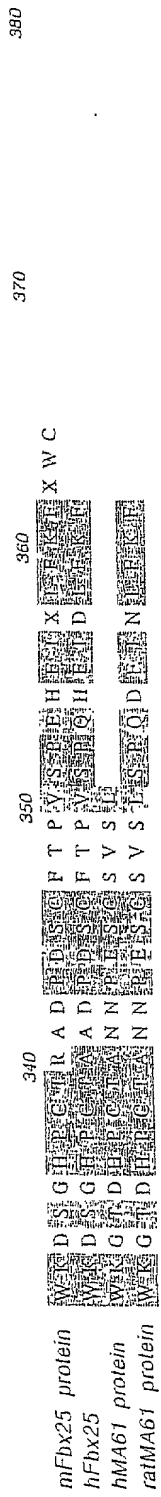


FIGURE 5B



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Figure 6

ATGGATTATAAATCTGGCTTGATTCCGGAACGGAAATGCTATGGAGAACCTGG
AGAAGCAGCTCATCTGCCCCATCTGCCTTGAGATGTTTACCAAGCCTGTGGT
CATCCTGCCCTGCCAGCACAACTCTGCCGGAAGTGTGCCAACGACATCTTC
CAGGCTGCCAATCCCTACTGGACCAACCGCGGTGGCTCGGTGTCCATGTCCTGG
AGGTGCTTTCCGCTGCCCCCTCGTGCCGCCATGAAGTGATCATGGACCGGCATG
GGGTGTACGGTCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTA
CAAGCAGGAATGCTCCAGTCGGCCCCCTGCAGAAAGGCAGCCACCCGATGTGC
AAGGAACACGAAGACGAGAAAATCAACATCTACTGTCTCACGTGCGAGGTG
CCTACTTGCTCCTTGTGCAAGGTGTTCCGGGGCTCACCCAGGCCTGTGAAGTTGC
CCCCTTACAAAGCATCTTCCAAGGACAGAAGACTGAACTGAGCAATTGCAT
CTCCATGCTGGTGGCAGGGAACGACCGAGTTCAGACTATCATCTCGCAGCTG
GAGGACTCCTGCCGAGTGACCAAGGAAAACAGCCACCAGGTGAAGGAGCAA
CTGAGCCACAAGTTTGACGCCCTCTACGCCATCCTGGACGAGAAGAAGAGTG
AGCTGCTGCAGCGGATCACTCAGGAGCAGGAGGAGAAGCTGGACTTCATCGA
GGCCCTGATCCTCCAGTACCGAGAGCAGTTGGAAAAGTCGACCAAGCTTGTG
GAAACAGCCATCCAGTCCCTGGATGAGCCCGGAGGGGGCCACCTTCCTCTTGA
GTGCCAAGCCGCTCATCAAGAGCATTGTAGAAGCTTCCAAGGGCTGCCAAGCT
GGGGAAGACAGAACAAGGCTTTGAGAACATGGACTACTTTACTCTGAATTT
AGAACACATAGCAGAGGCCTTGAGGGCCATCGACTTTGGGACAGATGAGGAG
GAGGAGTTTACTGAAGAGGAGGAGGAGGAGGATCAAGAAGAGGGCGTGTCC
ACAGAGGGGACACCAA

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Figure 7

MDYKSGLPDGNAMENLEKQLICPICLEMFTKPVVILPCQHNLCRKCANDIFQAAN
PYWTNRGGSVSMMSGGRFRCPSCORHEVIMDRHGVYGLQRNLLVENIIDYKQECSS
RPLQKGSHPMCKEHEDEKINIYCLTCEVPTCSLCKVFGAHQACEVAPLQSIFQGG
KTELSNCISMLVAGNDRVQTIISQLEDSCRVTKENSHQVKEELSHKFDALYAILDE
KKSELLQRITQEQQEELDFIEALILQYREQLEKSTKLVETAIQSLDEPGGATFLLSA
KPLIKSIVEASKGCQLGKTEQGFENMDYFTLNLEHIAEALRAIDFGTDEEEEFTEEE
EEEDQEEGVSTEGHQ

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Figure 8A

10 20 30 40 50
TTCTCAGGTACTTTATCGGACCTCTCACATGGCTGCATGCCAGAAATGT

60 70 80 90 100
GATGATATTGTTGACAGCCTCTTCAAGGGTTTGGTAGAACTGAGGGCAA

110 120 130 140 150
AGGTTTCCTCTTTCTCAAAGGTATCTCCACCTCTTCCCAAGCAGCAGCA

160 170 180 190 200
AAGTTAGGCTGACCTCGTCTGTTATGTAAAGGATGCGTAGGGATGGGAGG

210 220 230 240 250
GCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGTTTCCAT

260 270 280 290 300
TTCCTGAGCGTCTGAGATGTTAGTATTAGTTAGTTTTGTTGTGAGTGTTA

310 320 330 340 350
GAATTCGGGCACCAGGAGAAGGAAGCCAACAGGATCCGACCCGGTGTTTT

360 370 380 390 400
GTGACAAAGGCAAGACCCCCAGGTCTACTTAGAGCAAAGTTAGTAGAGGA

410 420 430 440 450
GGCAGCTAGGCGTGGCTCTCATTCCTTCCCACAGAATGGATTATAAGTCG

460 470 480 490 500
AGCCTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGAT

510 520 530 540 550
CTGCCCTATCTGCCTGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGT

560 570 580 590 600
GCCAGCACAACTGTGCCGGAAGTGTGCCAATGACATCTTCCAGGCTGCA

610 620 630 640 650
AATCCCTACTGGACCAGCCGGGCAGCTCAGTGTCATGTCTGGAGGCCG

660 670 680 690 700
TTTCCGCTGCCCCACCTGCCGCCACGAGGTGATCATGGATCGTCACGGAG

710 720 730 740 750
TGTACGGCCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTAC

760 770 780 790 800
AAACAGGAGTGCTCCAGTCGGCCGCTGCAGAAGGGCAGTCACCCCATGTG

810 820 830 840 850
CAAGGAGCACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGG

860 870 880 890 900
TGCCACCTGCTCCATGTGCAAGGTGTTTGGGATCCACAAGGCCTGCGAG

910 920 930 940 950
GTGGCCCCATTGCAGAGTGTCTTCCAGGGACAAAAGACTGAACTGAATAA

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Figure 8B

960 970 980 990 1000
CTGTATCTCCATGCTGGTGGCGGGGAATGACCGTGTGCAGACCATCATCA

1010 1020 1030 1040 1050
CTCAGCTGGAGGATTCCCGTCGAGTGACCAAGGAGAACAGTCACCAGGTA

1060 1070 1080 1090 1100
AAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGA

1110 1120 1130 1140 1150
GAAGAAAAGTGAGTTGCTGCAGCGGATCACGCAGGAGCAGGAGGAAAAGC

1160 1170 1180 1190 1200
TTAGCTTCATCGAGGCCCTCATCCAGCAGTACCAGGAGCAGCTGGACAAG

1210 1220 1230 1240 1250
TCCACAAAAGCTGGTGGAAACTGCCATCCAGTCCCTGGACGAGCCTGGGGG

1260 1270 1280 1290 1300
AGCCACCTTCCTCTTGACTGCCAAGCAACTCATCAAAAGCATTGTGGAAG

1310 1320 1330 1340 1350
CTTCCAAGGGCTGCCAGCTGGGGAAGACAGAGCAGGGCTTTGAGAACATG

1360 1370 1380 1390 1400
GACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCAT

1410 1420 1430 1440 1450
TGACTTTGGGACAGATGAGGAAGAGGAAGAATTCATTGAAGAAGAAGATC

1460 1470 1480 1490 1500
AGGAAGAGGAAGAGTCCACAGAAGGGAAGGAAGAAGGACACCAGTAAGGA

1510 1520 1530 1540 1550
GCTGGATGAATGAGAGGCCCCAGATGCAGAGAGACTGGAGAGGGTGGGG

1560 1570 1580 1590 1600
AGGGGCCCAGCGGCCCTGGTGACAGGCCAGGGTGGGAGGGGTCGGGGCC

1610 1620 1630 1640 1650
CCTGGAGGGGCAATGGGGAGGTGATGTCTTCTCTCTGCTCAGAGAGCAGG

1660 1670 1680 1690 1700
GACTAGGGTAGGACCCCTACCGCTGCGTCCAGCAGACACTGAACCAGAAT

1710 1720 1730 1740 1750
TGGAAACGTGCTTGAAACAATCACACAGGACACTTTTCTACATTGGTGCA

1760 1770 1780 1790 1800
AAATGGAATATTTTGTACATTTTAAATGTGATTTTGTATATACTTGT

1810 1820 1830 1840 1850
ATATGTATGCCAATTTGGTGCTTTTGTAAAGGAACCTTTGTATAATAAT

1860 1870 1880 1890 1900
GCCTGGTTCGTTGGGTGACCTGCGATTGTCTAGAAAGAGGGGAAGGAAGCCA

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Figure 8C

1910	1920	1930	1940	1950
GGTTGATACAGCTGCCCCACTTCCTTTCCTGAGCAGGAGGATGGGGTAGCA				
1960	1970	1980	1990	2000
CTCACAGGGACGATGTGCTGTATTTTCAGTGCCTATCCCAGACATACGGGG				
2010	2020	2030	2040	2050
TGGTAACTGAGTTTGTGTTATATGTTGTTTAAATAAATGCACAATGCTCT				
2060	2070	2080	2090	
CTTCCTGTTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				

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Figure 8C

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Figure 9

MENLEKQLICPICLEMFTKPVVILPCQHNLCKRCANDIFQAANPYWTSRGSSVSM
SGGRFRCPTCRHEVIMDRHGVYGLQRNLLVENIIDYKQECSSRPLQKGSHPMCK
EHEDKINIYCLTCEVPTCSMCKVFGIHKACEVAPLQSVFQGQKTELNNCISMLV
AGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDLYAILDEKKSELLQRITQE
QEEKLSFIEALIQYQEQLDKSTKLVETAIQSLDEPGGATFLLTAKQLIKSIVEASK
GCQLGKTEQGFENMDFFTLDEHIADALRAIDFGTDEEEEFIEEEDQEEESTEG
KEEGHQ

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Figure 9
MENLEKQLICPICLEMFTKPVVILPCQHNLCKRCANDIFQAANPYWTSRGSSVSM
SGGRFRCPTCRHEVIMDRHGVYGLQRNLLVENIIDYKQECSSRPLQKGSHPMCK
EHEDKINIYCLTCEVPTCSMCKVFGIHKACEVAPLQSVFQGQKTELNNCISMLV
AGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDLYAILDEKKSELLQRITQE
QEEKLSFIEALIQYQEQLDKSTKLVETAIQSLDEPGGATFLLTAKQLIKSIVEASK
GCQLGKTEQGFENMDFFTLDEHIADALRAIDFGTDEEEEFIEEEDQEEESTEG
KEEGHQ

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GACCTCAGCAGTTACTGCAACAAGGAGAATCTGTTCAACAGCCTGAACTAC
GATGTTGCAGCCAAGAAGAGAAAAGAAAGACATACAGAACAGCAAAACCAA
AACTCAGTATTTCCATCAGGAGAAGTGGATCTATGTTACAAAAGGGAGTAC
TAAGGAGCGCCATGGATACTGCACTTTGGGGGAAGCTTTCAACAGACTG GAC
TTCTCGACTGCCATCCTGGATTCCAGAAGATTCAACTACGTAGTAAGGCTGT
TGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATCGCCCCAAA
GAACTTCATGAACATTTTGGAAAAAGTAGTACTGAAAGTTCTTGAAGACCA
GCAAAACATAAGACTCATAACGGGAACCTTCTCCAGACCCCTCTACACATCCTT
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ATGTGGGTGTATCGAATGGAGACCACTCTACACTGGCAACAGCAGCTGAACA
GCATCCAGATCAGCAGGCGCGCCTTCAAAGGTCTCAGATCACCGACCTGCC
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GTCAGCCTGGGCCAGGCAGCCCCAGACCTGCATGTGCTCAGTGAAGACCGGC
TACTGTGGAAGAGACTCTGCCAGTACCACTTCTCAGAGCGGCAGATCCG CAA
GCGATTGATCTTGTCTGACAAAGGGCAGCTGGATTGGAAGAAGATGTACTTTT
AAGCTTGTGCGATGTTACCCAAGAAGAGAACAGTATGGGGTCACCCCTGCAGC
TTTGCAAACACTGCCACATTCTCTCCTGGAAGGGCACTGACCATCCATG CAC
GGCCAACAACCCAGAGAGCTGCTCCGTCTCACTTTCACCCCAAGACTTT ATT
AACTTGTTCAAGTTC

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LDSRRFNYVVRLLLEIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNIRLIRELL
QTLYTSLOTLVQRVGKSVLVGNINMWVYRMETTLHWQQQLNSIQISRPAFKGLTI
TDLPVCLQLNIMQRLSDGRDLVSLGQAAPDLHVLSEDRLLWKRLCQYHFSEKQIR
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LDSRRFNYVVRLLLEIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNIRLIRELL
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TDLPVCLQLNIMQRLSDGRDLVSLGQAAPDLHVLSEDRLLWKRLCQYHFSEKQIR
KRLILSDKGQLDWKKMYFKLVRCYPRREQYGVTLQLCKHCHILSWKGTDPCTAN
NPESCSVSLSPQDFINLFKF

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CGACCTCAGCAGTTACTGCAACAAGGAGGTATACAATAAGGAGAATCTTTT
CAACAGCCTGAACTATGATGTTGCAGCCAAGAAGAGAAAGAAGGACATGCT
GAATAGCAAAAACCAAACTCAGTATTTCCACCAAGAAAAATGGATCTATGT
TCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTGGGGGAA GC
TTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTT AAC
TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCC TGA
GTGGCATCGCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACT GA
AAGTCCTTGAAGACCAGCAAAACATTAGACTAATAAGGGAACTACTCC AGA
CCCTCTACACATCCTTATGTACACTGGTCCAAAGAGTCGGCAAGTCTGT GCT
GGTCGGGAACATTAACATGTGGGTGTATCGGATGGAGACGATTCTCCAC TGG
CAGCAGCAGCTGAACAACATTGATCACCAGGCCTGCCTTCAAAGGCC TCA
CCTTCACTGACCTGCCTTTGTGCCTACAACCTGAACATCATGCAGAGGCT GAG
CGACGGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCCGACCTGCACG TGC
TCAGCGAAGACCGGCTGCTGTGGAAGAACTCTGCCAGTACCACTTCTC CGA
GCGGCAGATCCGCAAACGATTAATTCTGTGACACAAAGGGCAGCTGGATT TGG
AAGAAGATGTATTTCAAACCTTGTCCGATGTTACCCAAGGAAAGAGCAG TAT
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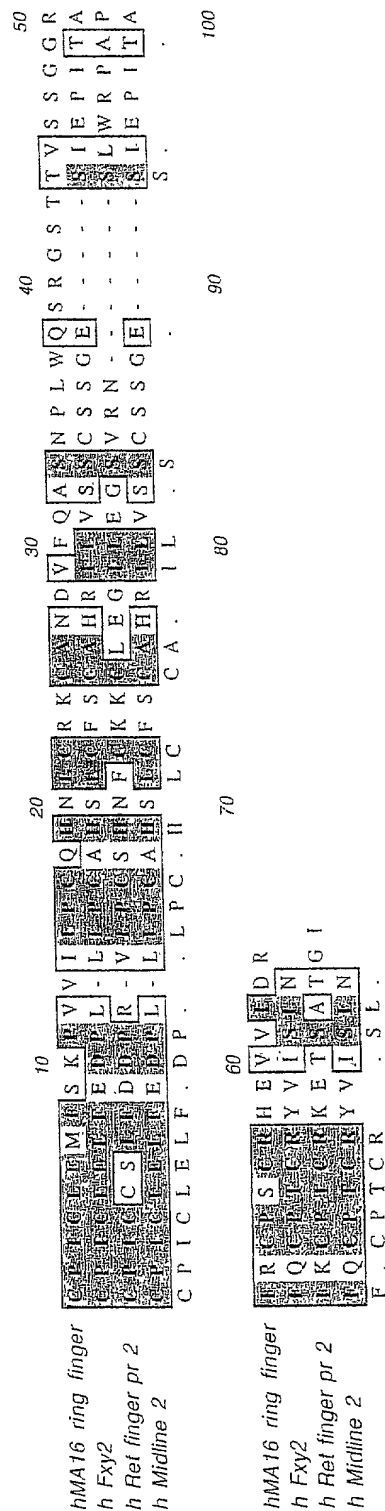
16/37
Figure 13

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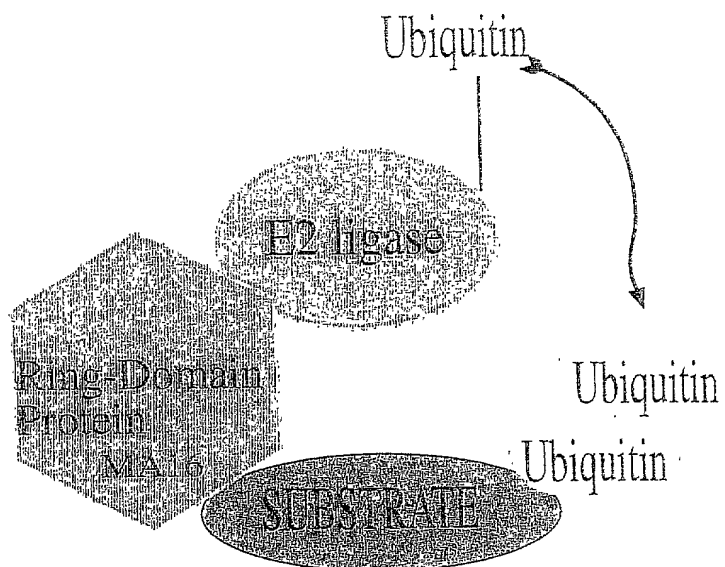
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RLIRELLQTLTYTSLCTLVQRVGKSVLVGNINMWVYRMETILHWQQQLNNIQIT RP
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DHPCTANNPESCSVSL

FIGURE 14

ClustalW Formatted Alignments



MA16 - A Monomeric Ring Ubiquitin Ligase



ATGGACTACAAAGACGATGACGACAAAGATTATAAATCTGGCTTGATTCCG
GACGGAAATGCTATGGAGAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCC
TTGAGATGTTTACCAAGCCTGTGGTCATCCTGCCCTGCCAGCACAACTCTG
CCGGAAGTGTGCCAACGACATCTTCCAGGCTGCCAATCCCTACTGGACCAAC
CGCGGTGGCTCGGTGTCCATGTCTGGAGGTCTGTTTCCGCTGCCCTCGTGC
CCATGAAGTGATCATGGACCGGCATGGGGTGTACGGTCTGCAGAGGAACCTG
CTGGTGGAGAACATCATCGACATCTACAAGCAGGAATGCTCCAGTCGGCCCC
TGCAGAAAGGCAGCCACCCGATGTGCAAGGAACACGAAGACGAGAAAAATCA
ACATCTACTGTCTCACGTGCGAGGTGCTACTTGTCTCCTTGTGCAAGGTGTT
GGGGCTCACCAGGCCTGTGAAGTTGCCCCCTTACAAAGCATCTTCCAAGGAC
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AGTTCAGACTATCATCTCGCAGCTGGAGGACTCCTGCCGAGTGACCAAGCTG
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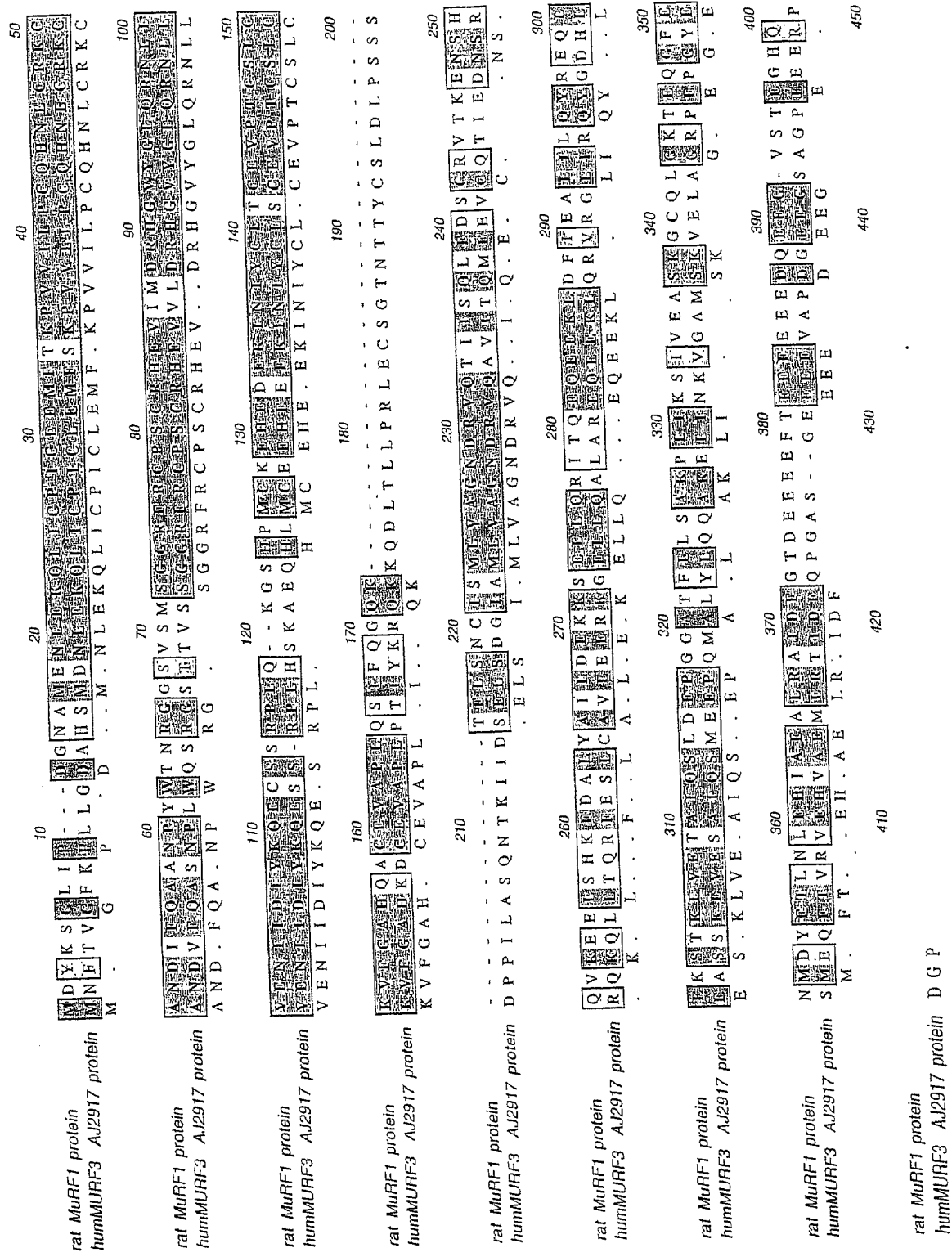
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ATGCCATTCTCGGGCAGGACTGGCGGTCCCCCGGGCAGAACTGGGTGAAGA
CGGCCGACGGCTGGAAGCGCTTCTGGATGAGAAGAGCGGCAGTTTCGTGAG
CGACCTCAGCAGTTACTGCAACAAGGAGGTATACAATAAGGAGAATCTTTT
CAACAGCCTGAACTATGATGTTGCAGCCAAGAAGAGAAAAGAAGGACATGCT
GAATAGCAAAACCAAACTCAGTATTTCCACCAAGAAAAATGGATCTATGT
TCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTGGGGGAA GC
TTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTT AAC
TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGA
GTGGCATCGCCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGA
AAGTCCTTGAAGACCAGCAAAACATTAGACTAATAAGGGAACTACTCCAGA
CCCTCTACACATCCTTATGTACACTGGTCCAAAGAGTCGGCAAGTCTGTGCT
GGTCGGGAACATTAACATGTGGGTGTATCGGATGGAGACGATTCTCCACTGG
CAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTCAAAGGCCCTCA
CCTTCACTGACCTGCCTTTGTGCCTACAACCTGAACATCATGCAGAGGCTGAG
CGACGGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCCGACCTGCACGTGC
TCAGCGAAGACCGGCTGCTGTGGAAGAACTCTGCCAGTACCACTTCTCCGA
GCGGCAGATCCGCAAACGATTAATTCTGTGACACAAAGGGCAGCTGGATTGG
AAGAAGATGTATTTCAAACCTTGTCCGATGTTACCCAAGGAAAGAGCAGTAT
GGAGATACCCTTCAGCTCTGCAAACACTGTCACATCCTTTCTGGAAGGGCA
CTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGCTCCGTTTCACTTTC
ACCCCAGGACTTTATCAACTTGTTCAAGTTC

Figure 19

MPFLGQDWRSPGQNWVKTADGWKRFLDEKSGSFVSDLSSYCNKEVYNKENLFN
SLNYDVAACKRKKDMLNSKTKTQYFHQEKWIYVHKGSTKERHGYCTLGEAFNRL
DFSTAILDSRRFNYYVRLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNI
RLIRELLQTLTSLCTLVQRVGKSVLVGNINMWVYRMETILHWQQQLNNIQITRP
AFKGLTFTDLPLCLQLNIMQRLSDGRDLVSLGQAAPDLHVLSEDRLLWKKLCQYH
FSERQIRKRLILSDKGQLDWKKMYFKLVRCYPRKEQYGDTLQLCKHCHILSWKGT
DHPCTANNPESCSVSLSPQDFINLFKF

Figure 20
ClustalW Formatted Alignments



ATGAAC TTCACAGTGGGTTTCAAGCCGCTGCTAGGGGATGCACACAGCATGG
ACAACCTGGAGAAGCAGCTCATCTGCCCATCTGCCTGGAGATGTTCTCCAA
ACCAGTGGTGATCCTGCCCTGCCAACACAACCTGTGCCGCCAAATGTGCCAAC
GACGTCTTCCAGGCCCTCGAATCCTCTATGGCAGTCCCGGGGGCTCCACCAC TGT
GTCTTCAGGAGGCCGTTTCCGCTGCCCATCGTGCAGGCATGAGGTTGTCTGG
ACAGACACGGGTGTCTACGGCCTGCAGCGAAACCTGCTAGTGGAGAACAT TAT
CGACATTTACAAGCAGGAGTCATCCAGGCCGCTGCACTCCAAGGCTGAGCAG
CACCTCATGTGCGAGGAGCATGAAGAAGAGAAGATCAATATTTACTGCC TG
AGCTGTGAGGTGCCACCTGCTCTCTCTGCAAGGTCTTCGGTGCCACAA GG
ACTGTGAGGTGGCCCCACTGCCACCATT TACAACGCCAGAAGAGTGA GCT
CAGCGATGGCATCGCGATGCTGGTGGCAGGCAATGACCGCGTGCAAGCAGTG
ATCACACAGATGGAGGAGGTGTGCCAGACTATCGAGGACAATAGCCGGA GGC
AGAAGCAGTTGTTAAACCAGAGGTTTGAGAGCCTGTGCGCAGTGCTGGA GGA
GCGCAAGGGTGAGCTGCTGCAGGCGCTGGCCCGGGAGCAAGAGGAGAAG CTG
CAGCGCGTCCGCGGCCCTCATCCGTCAGTATGGGACCCACCTGGAGGCCCTC TC
TAAGCTGGTGGAGTCTGCCATCCAGTCCATGGAAGAGCCACAAATGGCG CTG
TATCTCCAGCAGGCCAAGGAGCTGATCAATAAG

[illegible]

FIGURE 24

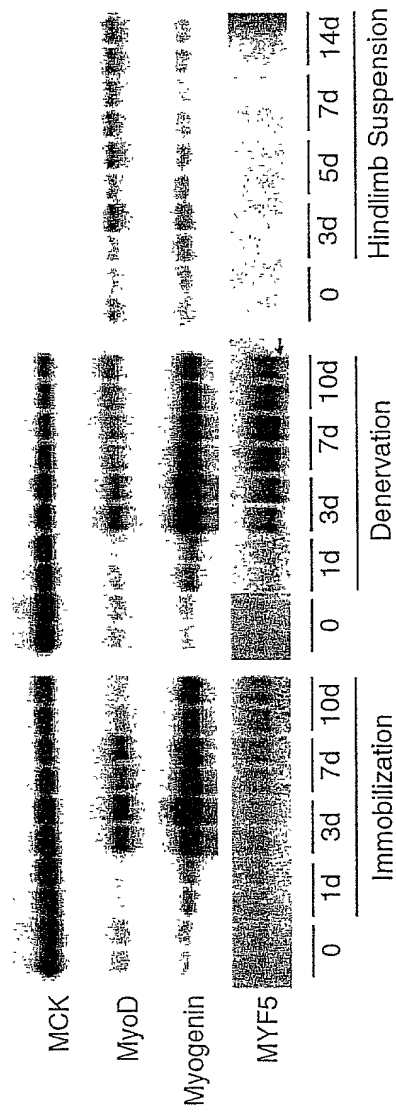


FIGURE 25A

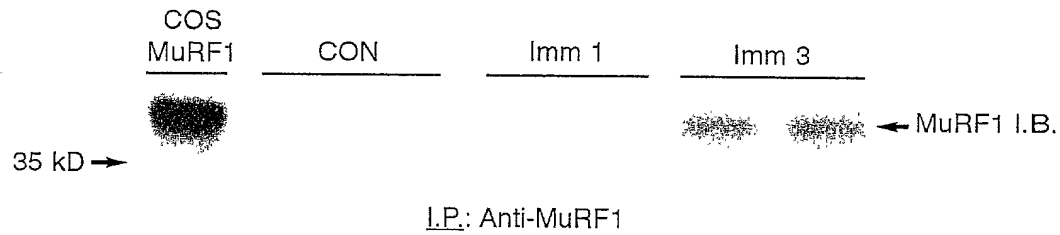


FIGURE 25B

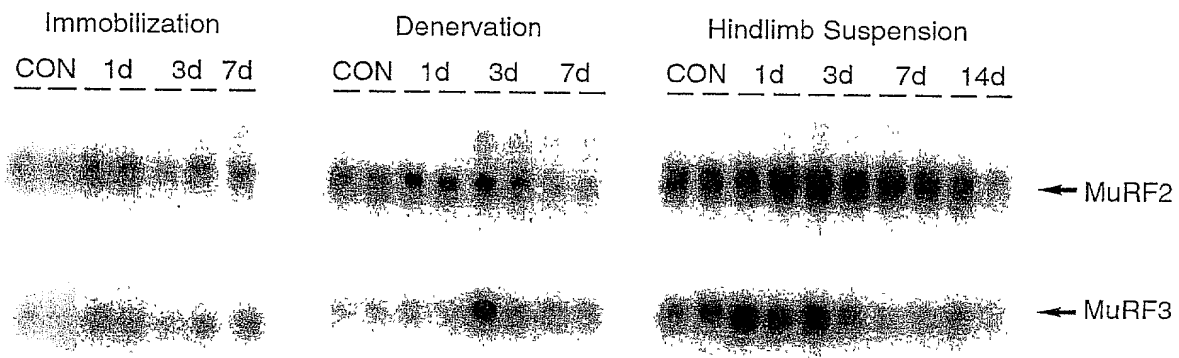


FIGURE 26

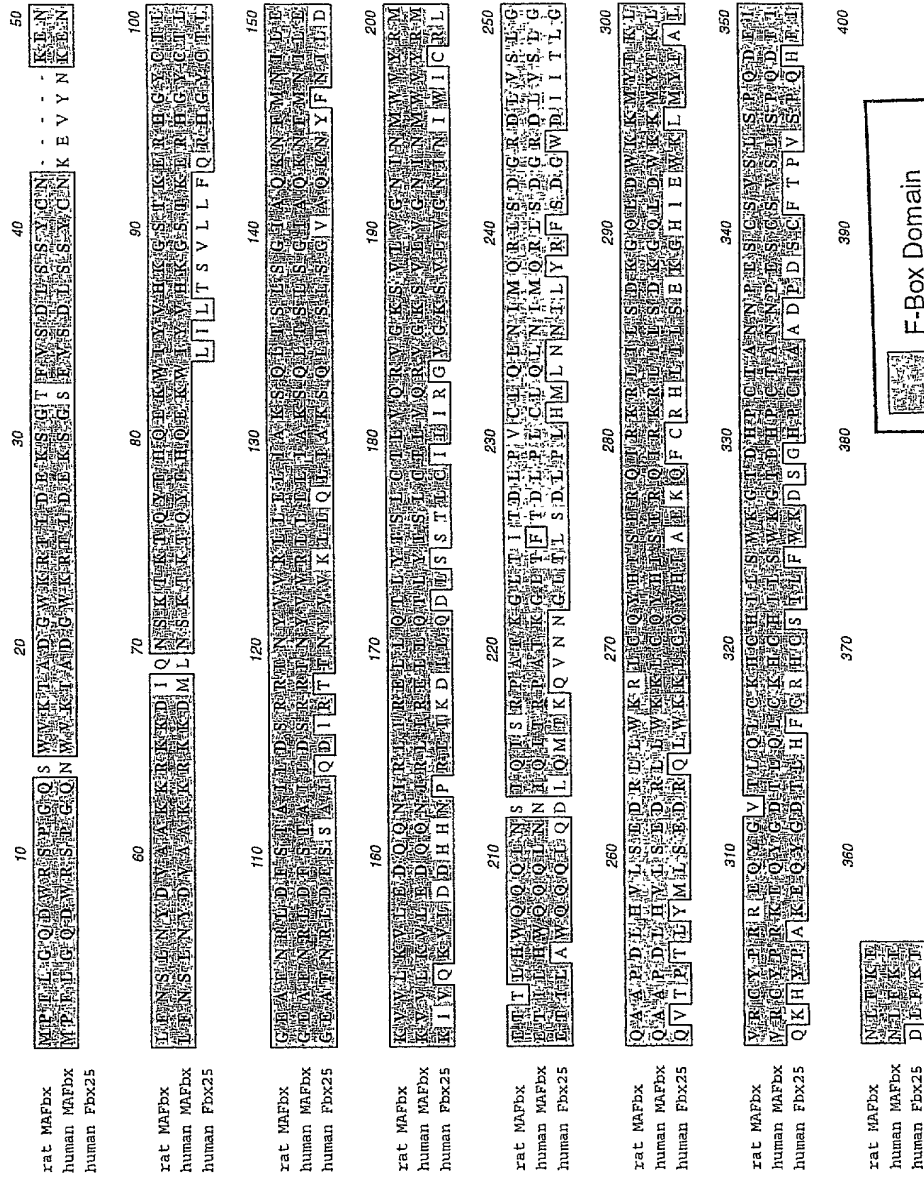


FIGURE 27A

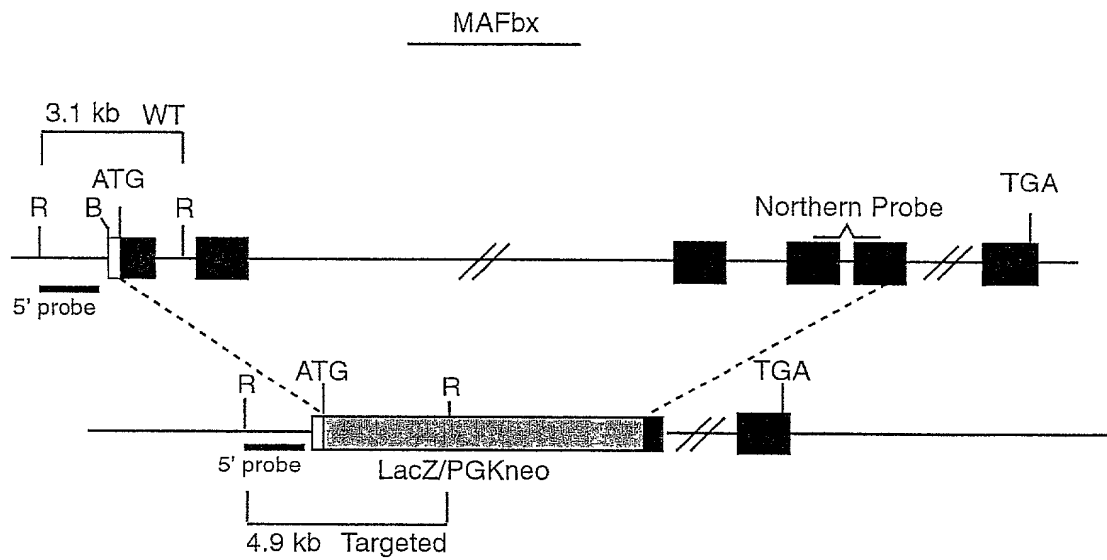


FIGURE 27B

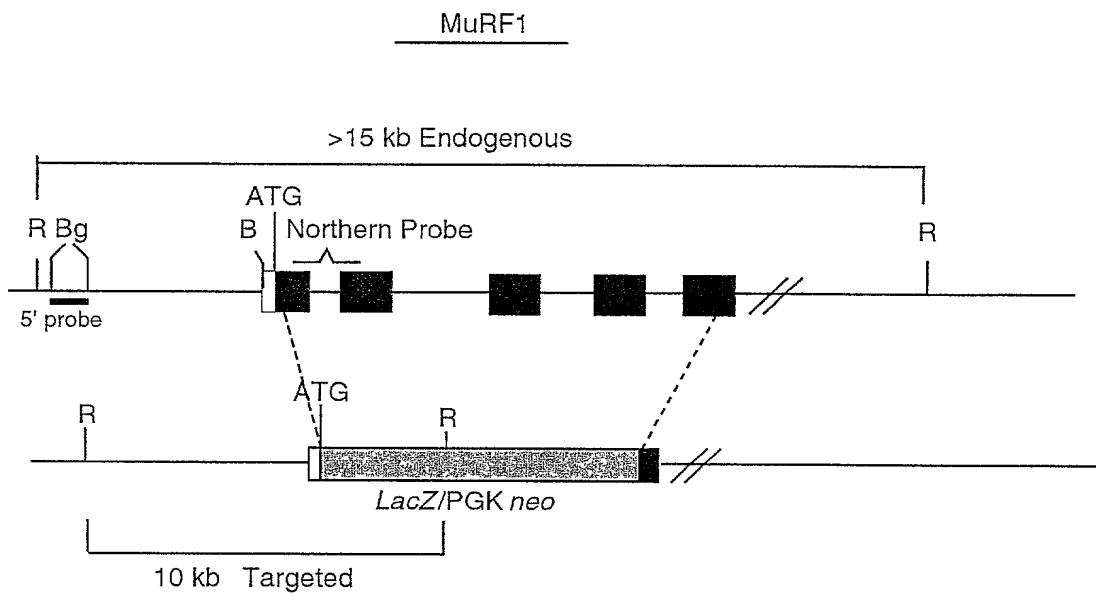


FIGURE 28A

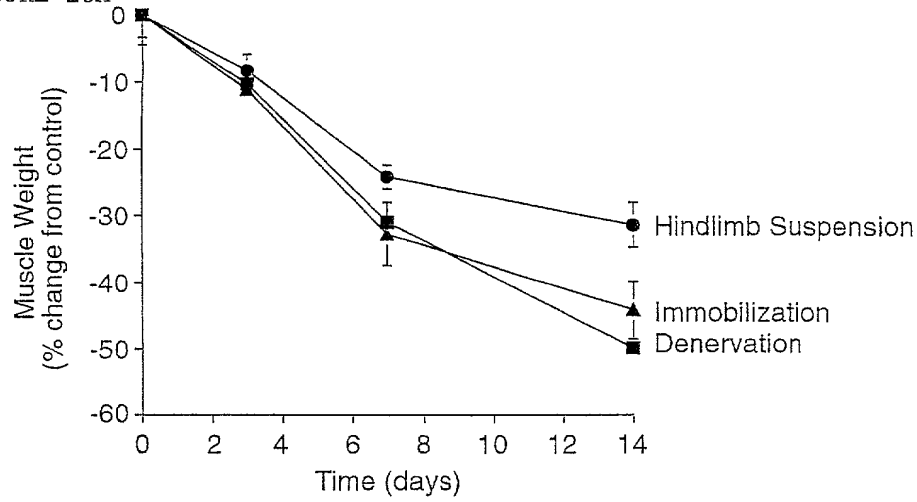


FIGURE 28B

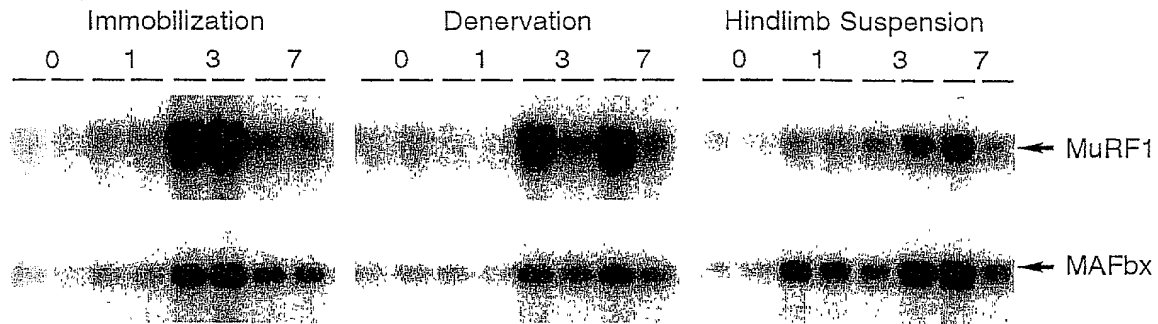


FIGURE 28C

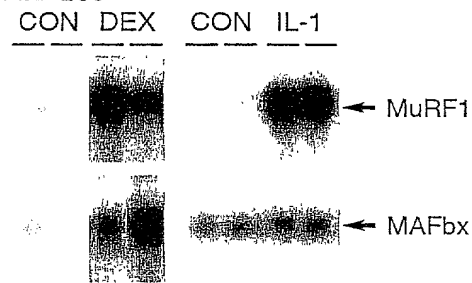


FIGURE 28D

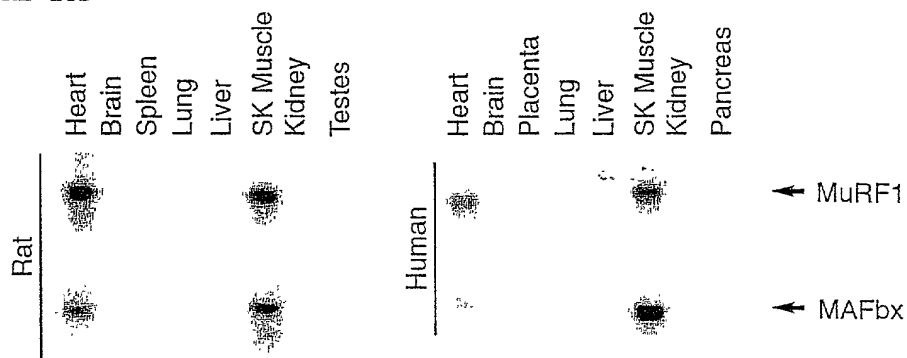


FIGURE 29A

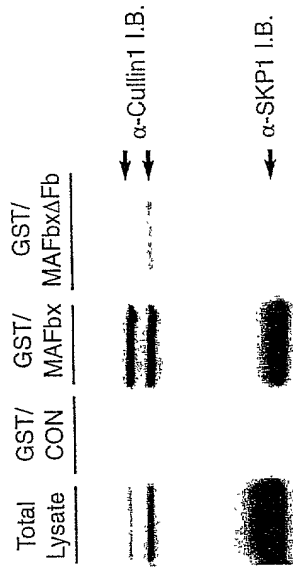


FIGURE 29C

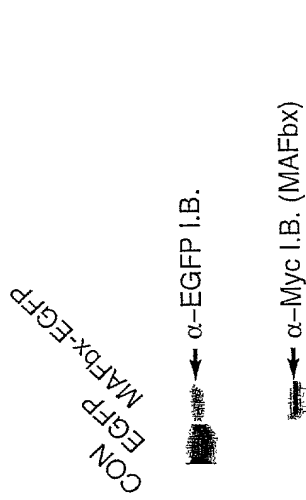


FIGURE 29B

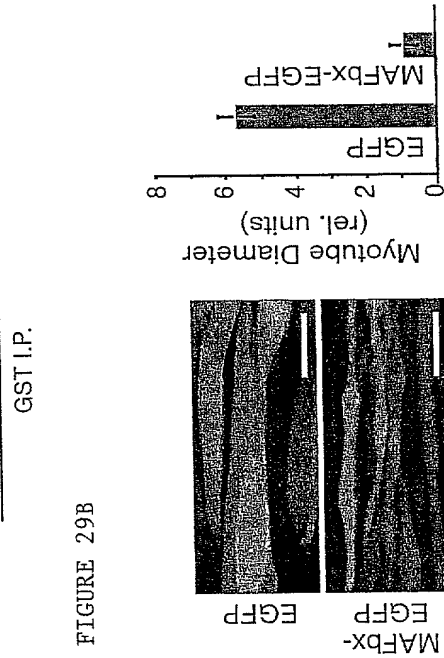


FIGURE 29D

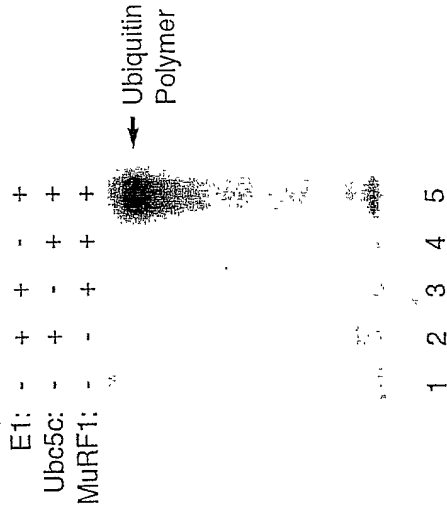


FIGURE 30A

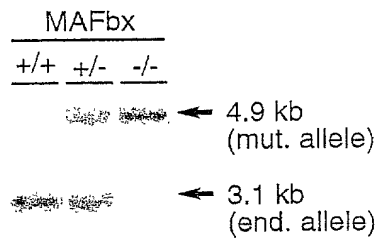


FIGURE 30C

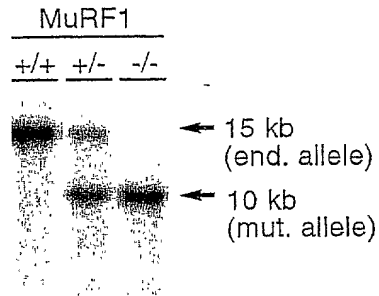


FIGURE 30B

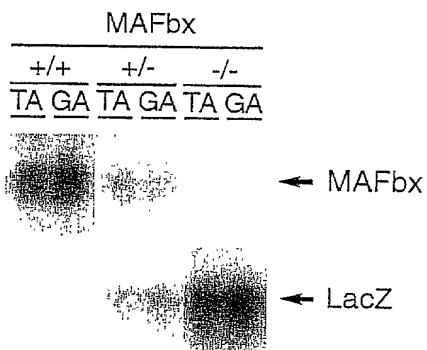


FIGURE 30D

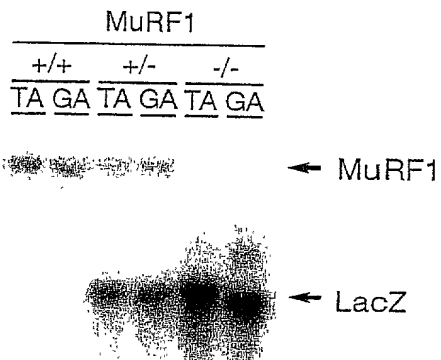


FIGURE 31A

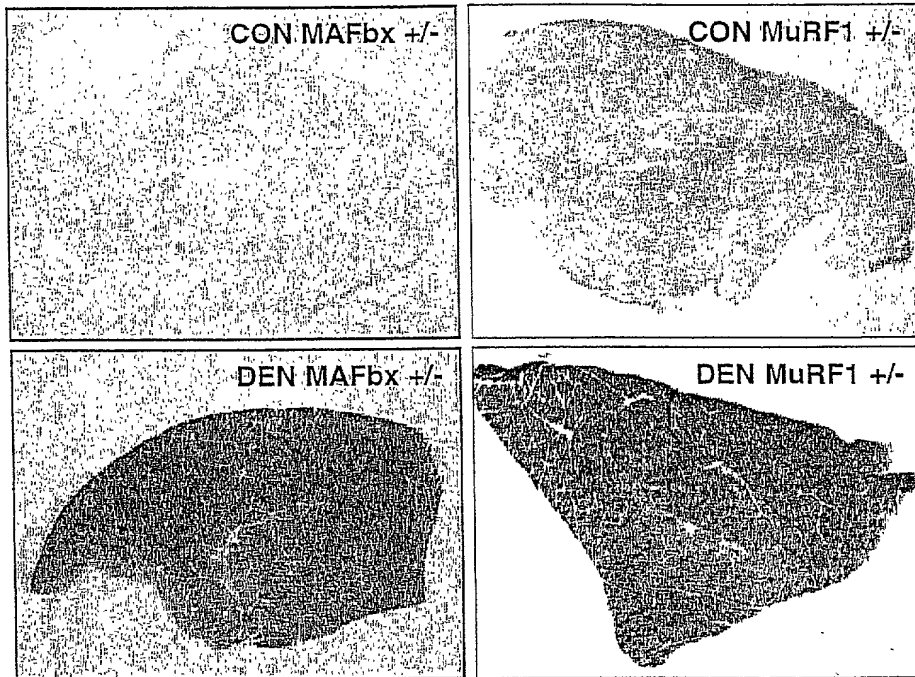


FIGURE 31B

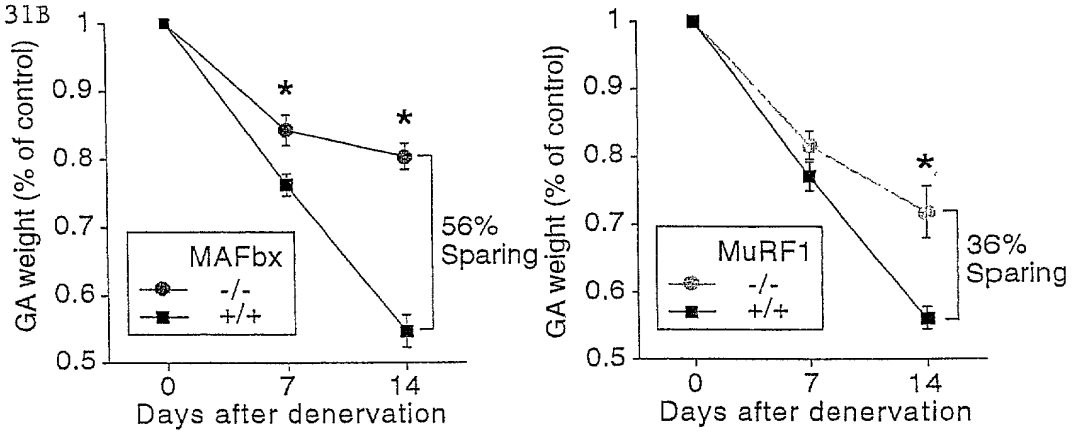


FIGURE 31C

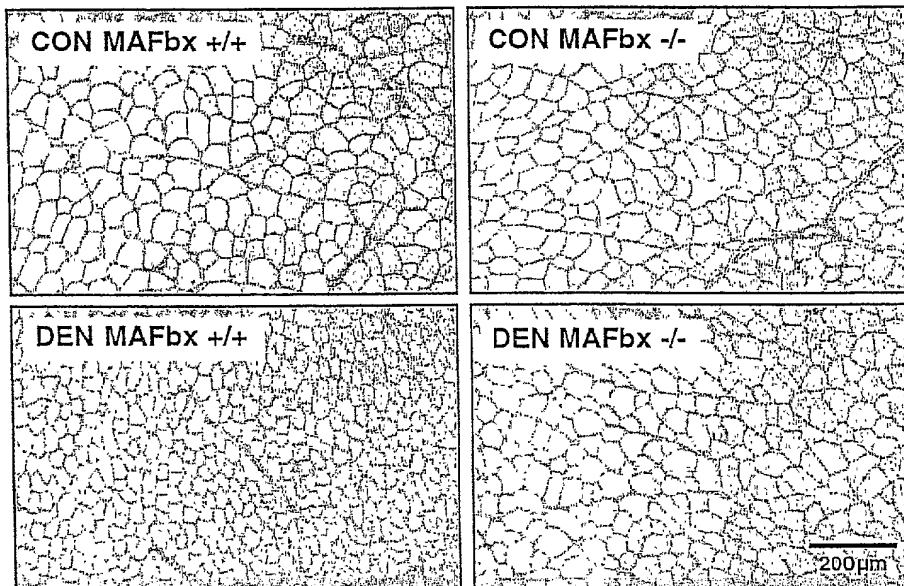


FIGURE 32

ClustalW Formatted Alignments

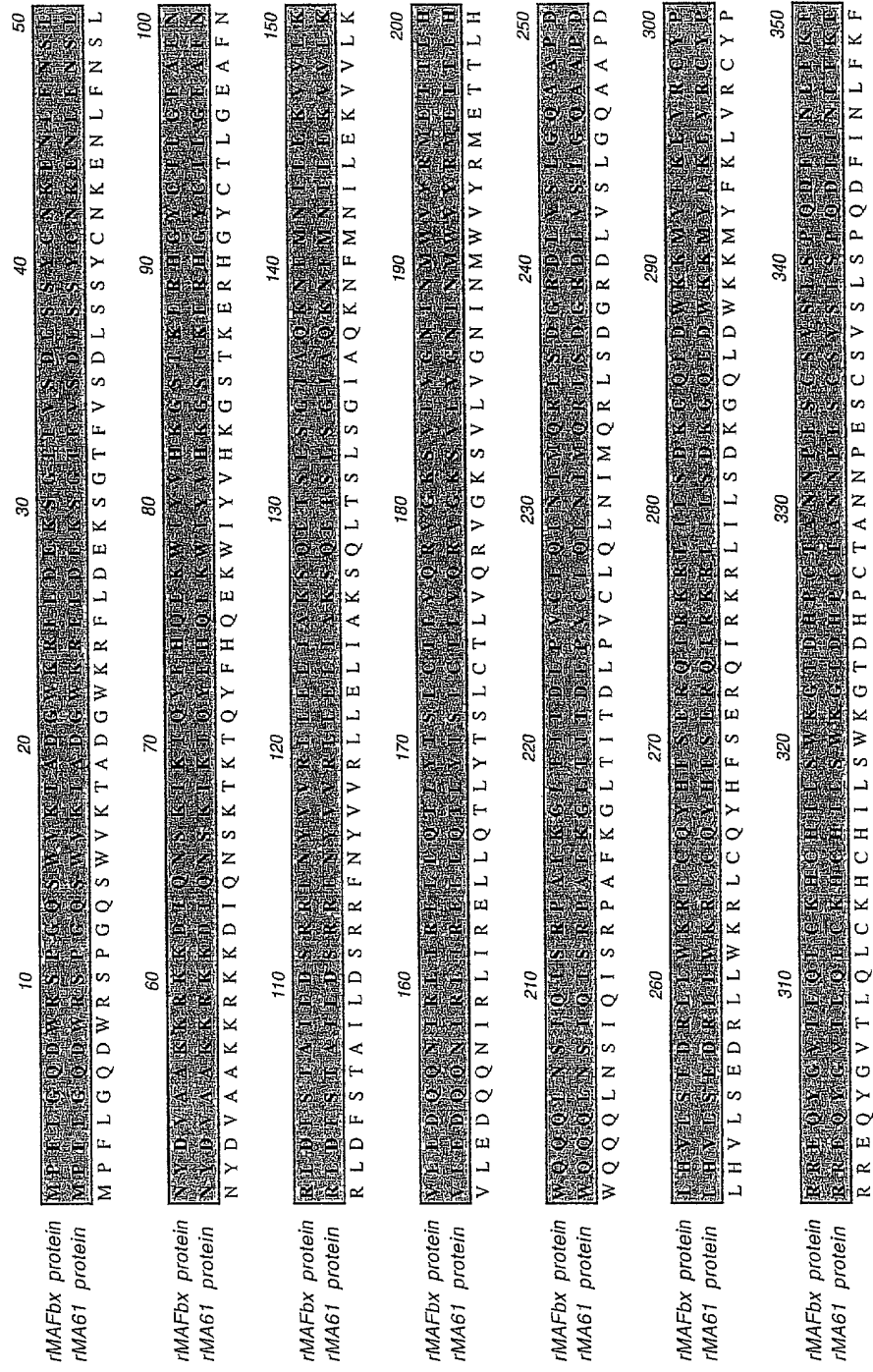


FIGURE 33

ClustalW Formatted Alignments

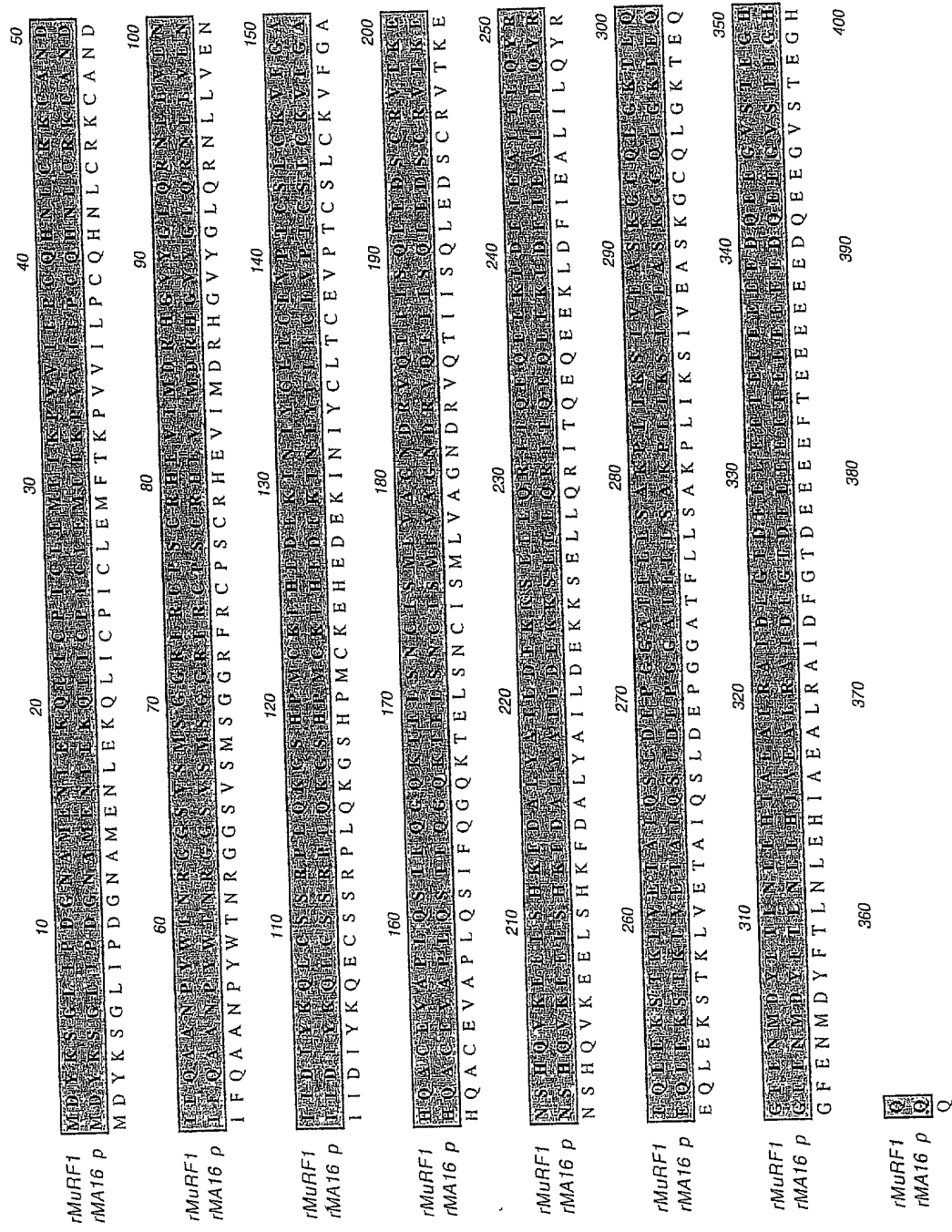


Figure 34
ClustalW Formatted Alignments

rMA16 protein humMURF1 protein	10	20	30	40	50
	M D Y K S G I L I P D G N A M E N L E K Q L I C P I C L E M F I A P V V I L P C Q H N L C R K C A N D				
	M D Y K S S L I Q D G N P M E N L E K Q L I C P I C L E M F I A P V V I L P C Q H N L C R K C A N D				
	M D Y K S L I D G N M E N L E K Q L I C P I C L E M F T K P V V I L P C Q H N L C R K C A N D				
rMA16 protein humMURF1 protein	60	70	80	90	100
	I L F Q A A N P Y W T N R G C S V S M S G G R F R C P S C R H E V I M D R H G V Y G L Q R N L L V E N				
	I L F Q A A N P Y W T S R G S S V S M S G G R F R C P T C R H E V I M D R H G V Y G L Q R N L L V E N				
	I F Q A A N P Y W T R G S V S M S G G R F R C P . C R H E V I M D R H G V Y G L Q R N L L V E N				
rMA16 protein humMURF1 protein	110	120	130	140	150
	I I D I Y K Q F C S S R P L O K G S H D M C K E H L D E K I N I Y C L T C E V P T C S . C K V F G A				
	I I D I Y K Q F C S S R P L O K G S H P M C K E H L D E K I N I Y C L T C E V P T C S M C K V L G I				
	I I D I Y K Q E C S S R P L Q K G S H P M C K E H D E K I N I Y C L T C E V P T C S . C K V F G				
rMA16 protein humMURF1 protein	160	170	180	190	200
	H Q A C E V A P L Q S I F O G Q K T E L S N C I S M L V A G N D R V Q T I I S Q L E D S R V T K E				
	H K A C E V A P L Q S V F O G Q K T E L N N C I S M L V A G N D R V Q T I I T O L E D S R V T K E				
	H . A C E V A P L Q S . F Q G Q K T E L N C I S M L V A G N D R V Q T I I . Q L E D S R V T K E				
rMA16 protein humMURF1 protein	210	220	230	240	250
	N S H Q V K E E L S H K T D I A L Y A I L D E K K S E L L Q R I T Q E Q E E K L D T L F A L I L Q Y R				
	N S H Q V K E E L S Q K F D T L Y A I L D E K K S E L L Q R I T Q E Q E E K L S T L F A L I L Q Y Q				
	N S H Q V K E E L S . K F D . L Y A I L D E K K S E L L Q R I T Q E Q E E K L F I E A L I Q Y .				
rMA16 protein humMURF1 protein	260	270	280	290	300
	E Q L E K S T K I V F E I A I O S L D E P P G G A T T L L S A K P L F K S I V E A S K G C Q L G K T E Q				
	E Q L D K S T K I V F E I A I O S L D E P P G G A T T L L T T A K Q L F K S I V E A S K G C Q L G K T E Q				
	E Q L . K S T K L V E T A I Q S L D E P P G G A T F L L . A K L I K S I V E A S K G C Q L G K T E Q				
rMA16 protein humMURF1 protein	310	320	330	340	350
	G F E N M D Y F T L N I F H I A E A I R A I D F G T D E F E L - T E E D Q E E G V S T				
	G F E N M D F T L D L L H I A D A L R A I D F G T D E F E E E E I E E D Q E E E S T L G K - E				
	G F E N M D . F T L L E H I A . A L R A I D F G T D E F E E E F E E E . E E E . E G				
rMA16 protein humMURF1 protein	360	370	380	390	400
	E G H Q				
	E G H Q				
	E G H Q				